

10 20 30 40 50 60  
CATCATCAATAATCTACAGTACACTGATGGCAGCGGTCCAACCTGCCAATCATTTTTTGCCA

70 80 90 100 110 120  
CGTCATTTATGACGCAACGACGGCGAGCGTGGCGTGCTGACGTAACGTGTGGGGCGGAGCG

130 140 150 160 170 180  
CGTCGCGGAGGCGGGCGGCGCTGGGCGGGGCTGAGGGCGGCGGGGGCGGCGCGGGGCGG

190 200 210 220 230 240  
CGCGCGGGGGCGGGGCGAGGGGCGGAGTTCCGCACCCGCTACGTCATTTTCAGACATTTTT

250 260 270 280 290 300  
TAGCAAATTTGCGCCTTTTGCAAGCATTTTCTCACATTTTCAGGTATTTAGAGGGCGGAT

310 320 330 340 350 360  
TTTTGGTGTTCGTA CTCCGTGTCACATAGTTCACTGTCAATCTTCATTACGGCTTAGAC

370 380 390 400 410 420  
AAATTTTCGGCGTCTTTTCCGGGTTTATGTCCCCGGTCACCTTTATGACTGTGTGAAACA

430 440 450 460 470 480  
CACCTGCCCATTTGTTTACCCTTGGTCAGTTTTTTCGTCTCCTAGGGTGGAACATCAAGA

490 500 510 520 530 540  
ACAAATTTGCCGAGTAATTGTGCACCTTTTTCCGCGTTAGGACTGCGTTTCACACGTAGA

550 560 570 580 590 600  
CAGACTTTTTCTCATTTTCTCAGACTCCGTCGTCCGCTTCAGAGCTCTGCGTCTTCGCTG

610 620 630 640 650 660  
CCACCATGAAGTACCTGGTCCTCGTTCTCAACGACGGCATGAGTCGAATTGAAAAGCTC  
MetLysTyrLeuValLeuValLeuAsnAspGlyMetSerArgIleGluLysAlaL

670 680 690 700 710 720  
TCCTGTGCAGCGATGGTGAGGTGGATTTAGAGTGTGATGAGGTACTTCCCCCTTCTCCCG  
euLeuCysSerAspGlyGluValAspLeuGluCysHisGluValLeuProProSerProA

730 740 750 760 770 780  
CGCCTGTCCCCGCTTCTGTGTACCCGCTGAGGAGTCCCTCCTCTGTCTCCGGTGTTTC  
laProValProAlaSerValSerProValArgSerProProProLeuSerProValPheP

790 800 810 820 830 840  
CTCCGTCTCCGCCAGCCCCGCTTGTGAATCCAGAGGCGAGTTCGCTGCTGCAGCAGTATC  
roProSerProProAlaProLeuValAsnProGluAlaSerSerLeuLeuGlnGlnTyrA

850 860 870 880 890 900  
GGAGAGAGCTGTTAGAGAGGAGCCTGCTCCGAACGGCCGAAGGTGAGCAGCGTGAGTGT  
rgArgGluLeuLeuGluArgSerLeuLeuArgThrAlaGluGlyGlnGlnArgAlaValC

910 920 930 940 950 960  
GTCCATGTGAGCGGTTGCCCGTGGAAGAGGATGAGTGTCTGAATGCCGTAAATTTGCTGT  
ysProCysGluArgLeuProValGluGluAspGluCysLeuAsnAlaValAsnLeuLeuP

FIGURE 1-1

970 980 990 1000 1010 1020  
TTCCTGATCCCTGGCTAAATGCAGCTGAAAATGGGGGTGATATTTTTTAAGTCTCCGGCTA  
heProAspProTrpLeuAsnAlaAlaGluAsnGlyGlyAspIlePheLysSerProAlaM

1030 1040 1050 1060 1070 1080  
TGTCTCCAGAACCGTGGATAGATTTGTCTAGCTACGATAGCGATGTAGAAGAGGTGACTA  
etSerProGluProTrpIleAspLeuSerSerTyrAspSerAspValGluGluValThrS

1090 1100 1110 1120 1130 1140  
GTCACCTTTTTTCTGGATTGCCCTGAAGACCCCAGTCGGGAGTGTTTCATCTTGTGGGTTTC  
erHisPhePheLeuAspCysProGluAspProSerArgGluCysSerSerCysGlyPheH

1150 1160 1170 1180 1190 1200  
ATCAGGCTCAAAGCGGAATTCAGGCATTATGTGCAGTTTGTGCTACATGCGCCAAACCT  
isGlnAlaGlnSerGlyIleProGlyIleMetCysSerLeuCysTyrMetArgGlnThrT

1210 1220 1230 1240 1250 1260  
ACCATTGCATCTATA(GTAAGTACATTCTGTAAAAGAACATCTTGGTGATTCTAGGTATT  
yrHisCysIleTyrS

1270 1280 1290 1300 1310 1320  
GTTTAGGGATTAACTGGGTGGAGTGATCTTAATCCGGCATAACCAAATACATGTTTTAC

1330 1340 1350 1360 1370 1380  
AGGTCCAGTTTCTGAAGAGGAAATGTGAGTCATGTTGACTTTGGCGCGC AAGAGGAAATG  
erProValSerGluGluGluMetEnd

1390 1400 1410 1420 1430 1440  
TGAGTCATGTTGACTTTGGCGCGCCCTACGGTGACTTTAAAGCAATTTGAGGATCACTTT

1450 1460 1470 1480 1490 1500  
TTTGTTAGTCGCTATAAAGTAGTCACGGAGTCTTCATGGATCACTTAAGCGTTCTTTTGG  
MetAspHisLeuSerValLeuLeuA

1510 1520 1530 1540 1550 1560  
ATTTGAAGCTGCTTCGCTCTATCGTAGCGGGGGCTTCAAATCGCACTGGAGTGTGGAAGA  
spLeuLysLeuLeuArgSerIleValAlaGlyAlaSerAsnArgThrGlyValTrpLysA

1570 1580 1590 1600 1610 1620  
GGCGGCTGTGGCTGGGACGCCTGACTCAACTGGTCCATGATACCTGCGTAGAGAACGAGA  
rgArgLeuTrpLeuGlyArgLeuThrGlnLeuValHisAspThrCysValGluAsnGluS

1630 1640 1650 1660 1670 1680  
GCATATTTCTCAATTCTCTGCCAGGGAATGAAGCTTTTTTAAGGTTGCTTCGGAGCGGCT  
erIlePheLeuAsnSerLeuProGlyAsnGluAlaPheLeuArgLeuLeuArgSerGlyT

1690 1700 1710 1720 1730 1740  
ATTTTGAAGTGTTTGACGTGTTTGTGGTGCCTGAGCTGCATCTGGACACTCCGGGTCGAG  
yrPheGluValPheAspValPheValValProGluLeuHisLeuAspThrProGlyArgV

FIGURE 1-2

1750 1760 1770 1780 1790 1800  
TGGTCGCCGCTCTTGCTCTGCTGGTGTTCATCCTCAACGATTTAGACGCTAATTCTGCTT  
alValAlaAlaLeuAlaLeuLeuValPheIleLeuAsnAspLeuAspAlaAsnSerAlaS  
1810 1820 1830 1840 1850 1860  
CTTCAGGCTTTGATTCAGGTTTTCTCGTGGACCGTCTCTGCGTGCCGCTATGGCTGAAGG  
MetAlaGluGl  
erSerGlyPheAspSerGlyPheLeuValAspArgLeuCysValProLeuTrpLeuLysA  
1870 1880 1890 1900 1910 1920  
CCAGGGCGTTCAAGATCACCCAGAGCTCCAGGAGCACTTCGCAGCCTTCCTCGTCGCCCCG  
yGlnGlyValGlnAspHisProGluLeuGlnGluHisPheAlaAlaPheLeuValAlaAr  
laArgAlaPheLysIleThrGlnSerSerArgSerThrSerGlnProSerSerSerProA  
1930 1940 1950 1960 1970 1980  
ACAAGACGACCCAGACTACCAGCCAGTAGACGGGGACAGCCCACCCCGGGCTAGCCTGGA  
gGlnAspAspProAspTyrGlnProValAspGlyAspSerProProArgAlaSerLeuGl  
spLysThrThrGlnThrThrSerGlnEnd  
1990 2000 2010 2020 2030 2040  
GGAGGCTGAACAGAGCAGCACTCGTTTTCGAGCACATCAGTTACCGAGACGTGGTGGATGA  
uGluAlaGluGlnSerSerThrArgPheGluHisIleSerTyrArgAspValValAspAs  
2050 2060 2070 2080 2090 2100  
CTTCAATAGATGCCATGATGTTTTTATGAGAGGTACAGTTTTGAGGACATAAAGAGCTA  
pPheAsnArgCysHisAspValPheTyrGluArgTyrSerPheGluAspIleLysSerTy  
2110 2120 2130 2140 2150 2160  
CGAGGCTTTGCCTGAGGACAATTTGGAGCAGCTCATAGCTATGCATGCTAAAATCAAGCT  
rGluAlaLeuProGluAspAsnLeuGluGlnLeuIleAlaMetHisAlaLysIleLysLe  
2170 2180 2190 2200 2210 2220  
GCTGCCCCGGTCGGGAGTATGAGTTGACTCAACCTTTGAACATAACATCTTGCGCCTATGT  
uLeuProGlyArgGluTyrGluLeuThrGlnProLeuAsnIleThrSerCysAlaTyrVa  
2230 2240 2250 2260 2270 2280  
GCTCGGAAATGGGGCTACTATTAGGGTAACAGGGGAAGCCTCCCCGGCTATTAGAGTGGG  
lLeuGlyAsnGlyAlaThrIleArgValThrGlyGluAlaSerProAlaIleArgValGl  
2290 2300 2310 2320 2330 2340  
GGCCATGGCCGTGGGTCCGTGTGTAACAGGAATGACTGGGGTGACTTTTGTGAATTGTAG  
yAlaMetAlaValGlyProCysValThrGlyMetThrGlyValThrPheValAsnCysAr  
2350 2360 2370 2380 2390 2400  
GTTTGAGAGAGAGTCAACAATTAGGGGGTCCCTGATACGAGCTTCAACTCACGTGCTGTT  
gPheGluArgGluSerThrIleArgGlySerLeuIleArgAlaSerThrHisValLeuPh  
2410 2420 2430 2440 2450 2460  
TCATGGCTGTTATTTTATGGGAATTATGGGCACTTGTATTGAGGTGGGGGCGGGAGCTTA  
eHisGlyCysTyrPheMetGlyIleMetGlyThrCysIleGluValGlyAlaGlyAlaTy

FIGURE 1-3

2044693.04402

2470 2480 2490 2500 2510 2520  
CATTTCGGGGTTGTGAGTTTGTGGGCTGTTACCGGGGAATCTGTTCTACTTCTAACAGAGA  
rIleArgGlyCysGluPheValGlyCysTyrArgGlyIleCysSerThrSerAsnArgAs

2530 2540 2550 2560 2570 2580  
TATTAAGGTGAGGCAGTGCACCTTTGACAAATGCTTACTGGGTATTACTTGTAAGGGGGA  
pIleLysValArgGlnCysAsnPheAspLysCysLeuLeuGlyIleThrCysLysGlyAs

2590 2600 2610 2620 2630 2640  
CTATCGTCTTTCGGGAAATGTGTGTTCTGAGACTTTCTGCTTTGCTCATTTAGAGGGAGA  
pTyrArgLeuSerGlyAsnValCysSerGluThrPheCysPheAlaHisLeuGluGlyGl

2650 2660 2670 2680 2690 2700  
GGGTTTGGTTAAAAACAACACAGTCAAGTCCCCTAGTCGCTGGACCAGCGAGTCTGGCTT  
uGlyLeuValLysAsnAsnThrValLysSerProSerArgTrpThrSerGluSerGlyPh

2710 2720 2730 2740 2750 2760  
TTCCATGATAACTTGTGCAGACGGCAGGGTTACGCCTTTGGGTTCCTCCACATTGTGGG  
eSerMetIleThrCysAlaAspGlyArgValThrProLeuGlySerLeuHisIleValGl

2770 2780 2790 2800 2810 2820  
CAACCGTTGTAGGCGTTGGCCAACCATGCAGGGGAATGTGTTTATCATGTCTAAACTGTA  
yAsnArgCysArgArgTrpProThrMetGlnGlyAsnValPheIleMetSerLysLeuTy

2830 2840 2850 2860 2870 2880  
TCTGGGCAACAGAATAGGGACTGTAGCCCTGCCCCAGTGTGCTTTCTACAAGTCCAGCAT  
rLeuGlyAsnArgIleGlyThrValAlaLeuProGlnCysAlaPheTyrLysSerSerIl

2890 2900 2910 2920 2930 2940  
TTGTTTGGAGGAGAGGGCGACAAACAAGCTGGTCTTGGCTTGTGCTTTTGAGAATAATGT  
eCysLeuGluGluArgAlaThrAsnLysLeuValLeuAlaCysAlaPheGluAsnAsnVa

2950 2960 2970 2980 2990 3000  
ACTGGTGTACAAAGTGCTGAGACGGGAGAGTCCCTCAACCGTGAAAATGTGTGTTTGTGG  
lLeuValTyrLysValLeuArgArgGluSerProSerThrValLysMetCysValCysGl

3010 3020 3030 3040 3050 3060  
GACTTCTCATTATGCAAAGCCTTTGACACTGGCAATTATTTCTTCAGATATTCGGGCTAA  
yThrSerHisTyrAlaLysProLeuThrLeuAlaIleIleSerSerAspIleArgAlaAs

3070 3080 3090 3100 3110 3120  
TCGATACATGTACACTGTGGACTCAACAGAGTTCCTTCTGACGAGGATTAAAAGTGGGC  
nArgTyrMetTyrThrValAspSerThrGluPheThrSerAspGluAspEnd

3130 3140 3150 3160 3170 3180  
GGGGCCAAGAGGGGTATAAATAGGTGGGGAGGTTGAGGGGAGCCGTAGTTTCTGTTTTTC

3190 3200 3210 3220 3230 3240  
CCAGACTGGGGGGGACAACATGGCCGAGGAAGGGCGCATTTATGTGCCTTATGTAAGTGC  
MetAlaGluGluGlyArgIleTyrValProTyrValThrAl

FIGURE 1-4

20446369400T

3250 3260 3270 3280 3290 3300  
CCGCCTGCCCAAGTGGTTCGGGTCGGTGCAGGATAAGACGGGCTCGAACATGTTGGGGGG  
aArgLeuProLysTrpSerGlySerValGlnAspLysThrGlySerAsnMetLeuGlyG1  
3310 3320 3330 3340 3350 3360  
TGTGGTACTCCCTCCTAATTCACAGGCGCACCGGACGGAGACCGTGGGCACTGAGGCCAC  
yValValLeuProProAsnSerGlnAlaHisArgThrGluThrValGlyThrGluAlaTh  
3370 3380 3390 3400 3410 3420  
CAGAGACAACCTGCACGCCGAGGGAGCGCGTCGTCCTGAGGATCAGACGCCCTACATGAT  
rArgAspAsnLeuHisAlaGluGlyAlaArgArgProGluAspGlnThrProTyrMetIl  
3430 3440 3450 3460 3470 3480  
CTTGGTGGAGGACTCTCTGGGAGGTTTGAAGAGGCGAATGGACTTGCTGGAAGAATCTAA  
eLeuValGluAspSerLeuGlyGlyLeuLysArgArgMetAspLeuLeuGluGluSerAs  
3490 3500 3510 3520 3530 3540  
TCAGCAGCTGCTGGCAACTCTCAACCGTCTCCGTACAGGACTCGCTGCCTATGTGCAGGC  
nGlnGlnLeuLeuAlaThrLeuAsnArgLeuArgThrGlyLeuAlaAlaTyrValGlnAl  
3550 3560 3570 3580 3590 3600  
TAACCTTGTGGGCGGCCAAGTTAACCCTTTGTTTAAATAAAAATACACTCATACAGTTT  
aAsnLeuValGlyGlyGlnValAsnProPheValEnd  
3610 3620 3630 3640 3650 3660  
ATTATGCTGTCAATAAAATTCTTTATTTTTCTGTGATAATACCGTGTCCAGCGTGCTCT  
3670 3680 3690 3700 3710 3720  
GTCAATAAGGGTCCTATGCATCCTGAGAAGGGCCTCATATACCCATGGCATGAATATTAA  
3730 3740 3750 3760 3770 3780  
GATACATGGGCATAAGGCCCTCAGAAGGGTTGAGGTAGAGCCACTGCAGACTTTCGTGGG  
3790 3800 3810 3820 3830 3840  
GAGGTAAGGTGTTGTAAATAATCCAGTCATACTGACTGTGCTGGGCGTGGAAGGAAAAGA  
3850 3860 3870 3880 3890 3900  
TGTCTTTTAGAAGAAGGGTGATTGGCAAAGGGAGGCTCTTAGTGTAGGTATTGATAAATC  
3910 3920 3930 3940 3950 3960  
TGTTCAAGTTGGGAGGGATGCATTCCGGGGGCTAATAAGGTGGAGTTTAGCCTGAATCTTAA  
3970 3980 3990 4000 4010 4020  
GGTTGGCAATGTTGCCCCCTAGGTCTTTGCGAGGATTCATGTTGTGCAGTACCACAAAAA  
4030 4040 4050 4060  
CAGAGTAGCCTGTGCATTTGGGGAATTTATCATGAAGCTT

FIGURE 1-5

ACTIVATION REGION

[illegible]

```

Ad5      175                                     189
TyrMetArgThrCys    GlyMetPheValTyrSerProValSerGluProGluProGlu
| | |              : | | | | | | | | | |
TyrMetArgGlnThrTyrHisCys  IleTyrSerProValSerGluGluGluMetEnd
BAV3     194                                     208

```

### Rb BINDING SEQUENCE

```

Ad5      120                                     132
         IleAspLeuThrCysHisGluAlaGlyPheProProSer
         :  |  |  |  |  |  |  |  |  |  |  |
BAV3     26                                     37
         ValAspLeuGluCysHisGluVal   LeuProProSer

```

```

Ad5          20                               26
GlnSerSerAsnSerThrSer
| | | | |
GlnSerSerArgSerThrSer
BAV3        136                               142

```

**FIGURE 3**

Ad5 150 GlnLysTyrSerIleGluGlnLeuThrThrTyrTrpLeuGlnProGlyAspAspPheGlu  
BAV3 74 GluArgTyrLysPheGluAspIleLysSerTyrGluAlaLeuProGluAspAsnLeuGlu  
170 GluAlaIleArgValTyrAlaLysValAlaLeuArgProAspCysLysTyrLysIleSer  
94 - GlnLeuIleAlaMetHisAlaLysIleLysLeuLeuProGlyArgGluTyrGluLeuThr  
190 LysLeuValAsnIleArgAsnCysCysTyrIleSerGlyAsnGlyAlaGluValGluIle  
114 GlnProLeuAsnIleThrSerCysAlaTyrValLeuGlyAsnGlyAlaThrIleArgVal  
210 AspThrGluAspArgValAlaPheArgCysSerMetIleAsnMetTrpProGlyValLeu  
134 ThrGlyGluAlaSerProAlaIleArgValGlyAlaMetAlaValGlyProCysValThr  
230 GlyMetAspGlyValValIleMetAsnValArgPheThr GlyProAsnPheSerGly  
154 GlyMetThrGlyValThrPheValAsnCysArgPheGluArgGluSerThrIleArgGly  
249 ThrValPheLeuAlaAsnThrAsnLeuIleLeuHisGlyValSerPheTyr GlyPhe  
174 SerLeuIleArgAlaSerThrHisValLeuPheHisGlyCys TyrPheMetGlyIle  
268 AsnAsnThrCysValGluAlaTrpThrAspValArgValArgGlyCysAlaPheTyrCys  
193 MetGlyThrCysIleGluValGlyAlaGlyAlaTyrIleArgGlyCysGluPheValGly  
288 CysTrpLysGlyValValCysArgProLysSerArgAla SerIleLysLysCysLeu  
213 CysTyrArgGlyIle CysSerThrSerAsnArgAspIleLysValArgGlnCysAsn  
307 PheGluArgCysThrLeuGlyIleLeuSerGluGlyAsnSerArgValArgHisAsnVal  
232 PheAspLysCysLeuLeuGlyIleThrCysLysGlyAspTyrArgLeuSerGlyAsnVal  
327 AlaSerAspCysGlyCysPheMetLeuValLysSerValAlaValIleLysHisAsnMet  
252 CysSerGluThrPheCysPheAlaHisLeuGluGlyGluGlyLeuValLysAsnAsnThr  
347 Val CysGlyAsn CysGluAspArgAlaSerGlnMetLeuThrCysSerAsp  
272 ValLysSerProSerArgTrpThrSerGluSerGlyPheSerMetIleThrCysAlaAsp  
364 GlyAsnCysHisLeuLeuLysThrIleHisVal AlaSerHisSerArgLysAlaTrp  
292 GlyArgValThrProLeuGlySerLeuHisIleValGlyAsnArgCysArgArg Trp  
383 ProValPheGluHisAsnIleLeuThrArgCysSerLeuHisLeuGlyAsnArgArgGly  
311 ProThrMetGlnGlyAsnValPheIleMetSerLysLeuTyrLeuGlyAsnArgIleGly  
403 ValPheLeuProTyrGlnCysAsnLeuSerHisThrLysIleLeuLeuGluProGlu  
331 ThrValAlaLeuPro GlnCysAlaPheTyrLysSerSerIleCysLeuGluGluArg  
422 SerMetSerLysValAsnLeuAsnGlyValPheAspMetThrMetLysIleTrpLysVal  
350 AlaThrAsnLysLeuValLeuAlaCysAlaPheGluAsnAsnValLeuValTyrLysVal  
442 LeuArgTyrAspGluThrArgThrArgCysArgProCysGluCysGlyGlyLysHisIle  
370 LeuArgArgGluSerProSerThr ValLysMetCysValCysGlyThrSerHisTyr  
462 ArgAsnGlnProValMetLeuAspVal ThrGluGluLeuArgProAspHisLeuVal  
389 AlaLysProLeuThrLeuAlaIleIleSerSerAspIleArgAlaAsnArgTyrMet  
481 LeuAlaCysThrArgAlaGluPheGlySerSerAspGluAspThrAspEnd  
408 TyrThrValAspSerThrGluPhe ThrSerAspGluAspEnd

FIGURE 4



FIGURE 5

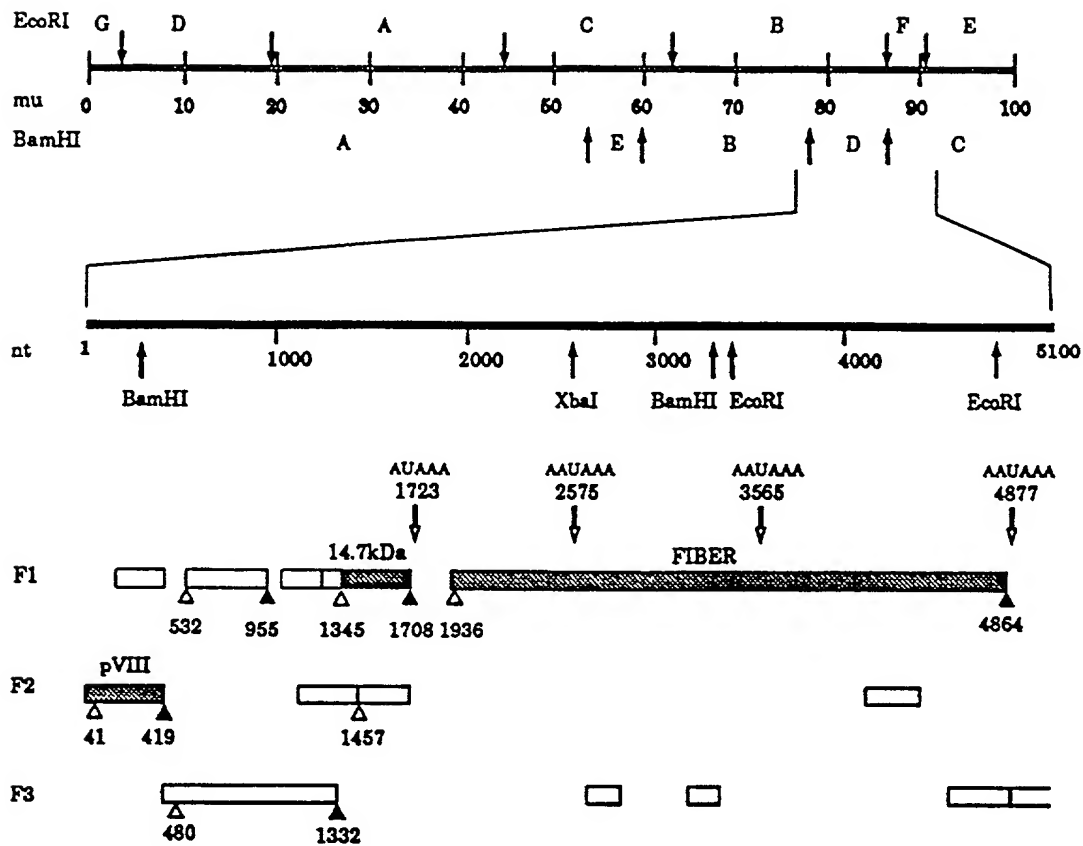


FIGURE 6

2044693-0140T

	10	20	30	40	50
C CTC ATC AAA CAA CCC GTG GTG GGC ACC ACC CAC GTG GAA ATG CCT CGC AAC					
ORF 1 Leu Ile Lys Gln Pro Val Val Gly Thr Thr His Val Glu Met Pro Arg Asn					
	60	70	80	90	100
GAA GTC CTA GAA CAA CAT CTG ACC TCA CAT GGC GCT CAA ATC GCG GGC GGA					
Glu Val Leu Glu Gln His Leu Thr Ser His Gly Ala Gln Ile Ala Gly Gly					
	110	120	130	140	150
GGC GCT GCG GGC GAT TAC TTT AAA AGC CCC ACT TCA GCT CGA ACC CTT ATC					
Gly Ala Ala Gly Asp Tyr Phe Lys Ser Pro Thr Ser Ala Arg Thr Leu Ile					
	160	170	180	190	200
CCG CTC ACC GCC TCC TGC TTA AGA CCA GAT GGA GTC TTT CAA CTA GGA GGA					
Pro Leu Thr Ala Ser Cys Leu Arg Pro Asp Gly Val Phe Gln Leu Gly Gly					
	210	220	230	240	250
GGC TCG CGT TCA TCT TTC AAC CCC CTG CAA ACA GAT TTT GCC TTC CAC GCC					
Gly Ser Arg Ser Ser Phe Asn Pro Leu Gln Thr Asp Phe Ala Phe His Ala					
	260	270	280	290	300
CTG CCC TCC AGA CCG CGC CAC GGG GGC ATA GGA TCC AGG CAG TTT GTA GAG					
Leu Pro Ser Arg Pro Arg His Gly Gly Ile Gly Ser Arg Gln Phe Val Glu					
	310	320	330	340	350
GAA TTT GTG CCC GCC GTC TAC CTC AAC CCC TAC TCG GGA CCG CCG GAC TCT					
Glu Phe Val Pro Ala Val Tyr Leu Asn Pro Tyr Ser Gly Pro Pro Asp Ser					
	360	370	380	390	400
TAT CCG GAC CAG TTT ATA CGC CAC TAC AAC GTG TAC AGC AAC TCT GTG AGC					
Tyr Pro Asp Gln Phe Ile Arg His Tyr Asn Val Tyr Ser Asn Ser Val Ser					
					ORF 2 Ala
410	420	430	440	450	460
GGT TAT AGC T GAG ATT GTA AGA CTC TCC TAT CTG TCT CTG TGC TGC TTT TCC					
Gly Tyr Ser					
Val Ile Ala Glu Ile Val Arg Leu Ser Tyr Leu Ser Leu Cys Cys Phe Ser					
	470	480	490	500	510
GCT TCA AGC CCC ACA AGC ATG AAG GGG TTT CTG CTC ATC TTC AGC CTG CTT					
Ala Ser Ser Pro Thr Ser Met Lys Gly Phe Leu Leu Ile Phe Ser Leu Leu					
	520	530	540	550	560
GTG CAT TGT CCC CTA ATT CAT GTT GGG ACC ATT AGC TTC TAT GCT GCA AGG					
ORF 3 Phe Met Leu Gly Pro Leu Ala Ser Met Leu Gln Gly					
Val His Cys Pro Leu Ile His Val Gly Thr Ile Ser Phe Tyr Ala Ala Arg					
	570	580	590	600	610
CCC GGG TCT GAG CCT AAC GCG ACT TAT GTT TGT GAC TAT GGA AGC GAG TCA					
Pro Gly Leu Ser Leu Thr Arg Leu Met Phe Val Thr Met Glu Ala Ser Gln					
Pro Gly Ser Glu Pro Asn Ala Thr Tyr Val Cys Asp Tyr Gly Ser Glu Ser					
	620	630	640	650	660
GAT TAC AAC CCC ACC ACG GTT CTG TGG TTG GCT CGA GAG ACC GAT GGC TCC					
Ile Thr Thr Pro Pro Arg Phe Cys Gly Trp Leu Glu Arg Pro Met Ala Pro					
Asp Tyr Asn Pro Thr Thr Val Leu Trp Leu Ala Arg Glu Thr Asp Gly Ser					

FIGURE 7-1

670 6P 690 7C 710  
TGG ATC TCT GTT C<sub>1</sub> TTC CGT CAC AAC GGC TCC TCA ACT GCA GCC CCC GGG  
Gly Ser Leu Phe Phe Ser Val Thr Thr Ala Pro Gln Leu Gln Pro Pro Gly  
Trp Ile Ser Val Leu Phe Arg His Asn Gly Ser Ser Thr Ala Ala Pro Gly

720 730 740 750 760  
GTC GTC GCG CAC TTT ACT GAC CAC AAC AGC AGC ATT GTG GTG CCC CAG TAT  
Ser Ser Arg Thr Leu Leu Thr Thr Thr Ala Ala Leu Trp Cys Pro Ser Ile  
Val Val Ala His Phe Thr Asp His Asn Ser Ser Ile Val Val Pro Gln Tyr

770 780 790 800 810  
TAC CTC CTC AAC AAC TCA CTC TCT AAG CTC TGC TGC TCA TAC CGG CAC AAC  
Thr Ser Ser Thr Thr His Ser Leu Ser Ser Ala Ala His Thr Gly Thr Thr  
Tyr Leu Leu Asn Asn Ser Leu Ser Lys Leu Cys Cys Ser Tyr Arg His Asn

820 830 840 850 860  
GAG CGT TCT CAG TTT ACC TGC AAA CAA GCT GAC GTC CCT ACC TGT CAC GAG  
Ser Val Leu Ser Leu Pro Ala Asn Lys Leu Thr Ser Leu Pro Val Thr Ser  
Glu Arg Ser Gln Phe Thr Cys Lys Gln Ala Asp Val Pro Thr Cys His Glu

870 880 890 900 910 920  
CCC GGC AAG CCG CTC ACC CTC CGC GTC TCC CCC GCG CTG GGA ACT GCC CAC  
Pro Ala Ser Arg Ser Pro Ser Ala Ser Pro Pro Arg Trp Glu Leu Pro Thr  
Pro Gly Lys Pro Leu Thr Leu Arg Val Ser Pro Ala Leu Gly Thr Ala His

930 940 950 960 970  
CAA GCA GTC ACT TGG TTT TTT CAA AAT GTA CCC ATA GCT ACT GTT TAC CGA  
Lys Gln Ser Leu Gly Phe Phe Lys Met Tyr Pro  
Gln Ala Val Thr Trp Phe Phe Gln Asn Val Pro Ile Ala Thr Val Tyr Arg

980 990 1000 1010 1020  
CCT TGG GGC AAT GTA ACT TGG TTT TGT CCT CCC TTC ATG TGT ACC TTT AAT  
Pro Trp Gly Asn Val Thr Trp Phe Cys Pro Pro Phe Met Cys Thr Phe Asn

1030 1040 1050 1060 1070  
GTC AGC CTG AAC TCC CTA CTT ATT TAC AAC TTT TCT GAC AAA ACC GGG GGG  
Val Ser Leu Asn Ser Leu Leu Ile Tyr Asn Phe Ser Asp Lys Thr Gly Gly

1080 1090 1100 1110 1120  
CAA TAC ACA GCT CTC ATG CAC TCC GGA CCT GCT TCC CTC TTT CAG CTC TTT  
Gln Tyr Thr Ala Leu Met His Ser Gly Pro Ala Ser Leu Phe Gln Leu Phe

1130 1140 1150 1160 1170  
AAG CCA ACG ACT TGT GTC ACC AAG GTG GAG GAC CCG CCG TAT GCC AAC GAC  
Lys Pro Thr Thr Cys Val Thr Lys Val Glu Asp Pro Pro Tyr Ala Asn Asp

1180 1190 1200 1210 1220  
CCG GCC TCG CCT GTG TGG CGC CCA CTG CTT TTT GCC TTC GTC CTC TGC ACC  
Pro Ala Ser Pro Val Trp Arg Pro Leu Leu Phe Ala Phe Val Leu Cys Thr

1230 1240 1250 1260 1270  
GGC TGC GCG GTG TTG TTA ACC GCC TTC GGT CCA TCG ATT CTA TCC GGT ACC  
Gly Cys Ala Val Leu Leu Thr Ala Phe Gly Pro Ser Ile Leu Ser Gly Thr  
ORF 4 Pro Pro Ser Val His Arg Phe Tyr Pro Val Pro

1280 1290 1300 1310 1320  
 CGA AAG CTT ATC TC GCC CGC TTT TGG AGT CCC G. CCC TAT ACC ACC CTC  
 Glu Ser Leu Ser Gln Pro Ala Phe Gly Val Pro Ser Pro Ile Pro Pro Ser  
 Arg Lys Leu Ile Ser Ala Arg Phe Trp Ser Pro Glu Pro Tyr Thr Thr Leu

1330 1340 1350 1360 1370 1380  
 CAC T AAC AGT CCC CCC ATG GAG CCA GAC GGA GTT CAT GCC GAG CAG CAG TTT  
 Thr Asn Ser Pro Pro Met Glu Pro Asp Gly Val His Ala Glu Gln Gln Phe  
 His

1390 1400 1410 1420 1430  
 ATC CTC AAT CAG ATT TCC TGC GCC AAC ACT GCC CTC CAG CGT CAA AGG GAG  
 Ile Leu Asn Gln Ile Ser Cys Ala Asn Thr Ala Leu Gln Arg Gln Arg Glu

1440 1450 1460 1470 1480  
 GAA CTA GCT TCC CTT GTC ATG TTG CAT GCC TGT AAG CGT GGC CTC TTT TGT  
 Glu Leu Ala Ser Leu Val Met Leu His Ala Cys Lys Arg Gly Leu Phe Cys  
 ORF 5 Leu Pro Leu Ser Cys Cys Met Pro Val Ser Val Ala Ser Phe Val

1490 1500 1510 1520 1530  
 CCA GTC AAA ACT TAC AAG CTC AGC CTC AAC GCC TCG GCC AGC GAG CAC AGC  
 Pro Val Lys Thr Tyr Lys Leu Ser Leu Asn Ala Ser Ala Ser Glu His Ser  
 Gln Ser Lys Leu Thr Ser Ser Ala Ser Thr Pro Arg Pro Ala Ser Thr Ala

1540 1550 1560 1570 1580  
 CTG CAC TTT GAA AAA AGT CCC TCC CGA TTC ACC CTG GTC AAC ACT CAC GCC  
 Leu His Phe Glu Lys Ser Pro Ser Arg Phe Thr Leu Val Asn Thr His Ala  
 Cys Thr Leu Lys Lys Val Pro Pro Asp Ser Pro Trp Ser Thr Leu Thr Pro

1590 1600 1610 1620 1630  
 GGA GCT TCT GTG CGA GTG GCC CTA CAC CAC CAG GGA GCT TCC GGC AGC ATC  
 Gly Ala Ser Val Arg Val Ala Leu His His Gln Gly Ala Ser Gly Ser Ile  
 Glu Leu Leu Cys Glu Trp Pro Tyr Thr Thr Arg Glu Leu Pro Ala Ala Ser

1640 1650 1660 1670 1680  
 CGC TGT TCC TGT TCC CAC GCC GAG TGC CTC CCC GTC CTC CTC AAG ACC CTC  
 Arg Cys Ser Cys Ser His Ala Glu Cys Leu Pro Val Leu Leu Lys Thr Leu  
 Ala Val Pro Val Pro Thr Pro Ser Ala Ser Pro Ser Ser Ser Arg Pro Ser

1690 1700 1710 1720 1730 1740  
 TGT GCC TTT AAC TTT TTA GAT TAG CTGAAAGCAA ATATAAAATG GTGTGCTTAC  
 Cys Ala Phe Asn Phe Leu Asp  
 Val Pro Leu Thr Phe

1750 1760 1770 1780 1790  
 CGTAATTCTG TTTTGACTTG TGTGCTTGA TTT CTC CCC CTG CGC CGT AAT CCA GTG

1800 1810 1820 1830 1840  
 CCC CTC TTC AAA ACT CTC GTA CCC TAT GCG ATT CGC ATA GGC ATA TTT TCT

1850 1860 1870 1880 1890  
 AAA AGC TCT GAA GTC AAC ATC ACT CTC AAA CAC TTC TCC GTT GTA GGT TAC

1900 1910 1920 1930 1940 1950  
 TTT CAT CTA CAG ATA AAG TCA TCC ACC GGT T AAC ATC ATG AAG AGA AGT GTG  
 ORF 6 Ser His Pro Pro Val Asn Ile Met Lys Arg Ser Val

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1960					1970					1980					1990					2000									
CCC	CAG	GAC	TTT	AA.	CTT	GTG	TAT	CCG	TAC	AAG	GC.	AAG	AGG	CCC	AAC	ATC													
Pro	Gln	Asp	Phe	Asn	Leu	Val	Tyr	Pro	Tyr	Lys	Ala	Lys	Arg	Pro	Asn	Ile													
2010					2020					2030					2040					2050									
ATG	CCG	CCC	TTT	TTT	GAC	CGC	AAT	GGC	TTT	GTT	GAA	AAC	CAA	GAA	GCC	ACG													
Met	Pro	Pro	Phe	Phe	Asp	Arg	Asn	Gly	Phe	Val	Glu	Asn	Gln	Glu	Ala	Thr													
2060					2070					2080					2090					2100									
CTA	GCC	ATG	CTT	GTG	GAA	AAG	CCG	CTC	ACG	TTC	GAC	AAG	GAA	GGT	GCG	CTG													
Leu	Ala	Met	Leu	Val	Glu	Lys	Pro	Leu	Thr	Phe	Asp	Lys	Glu	Gly	Ala	Leu													
2110					2120					2130					2140					2150									
ACC	CTG	GGC	GTC	GGA	CGC	GGC	ATC	CGC	ATT	AAC	CCC	GCG	GGG	CTT	CTG	GAG													
Thr	Leu	Gly	Val	Gly	Arg	Gly	Ile	Arg	Ile	Asn	Pro	Ala	Gly	Leu	Leu	Glu													
2160					2170					2180					2190					2200									
ACA	AAC	GAC	CTC	GCG	TCC	GCT	GTC	TTC	CCA	CCG	CTG	GCC	TCC	GAT	GAG	GCC													
Thr	Asn	Asp	Leu	Ala	Ser	Ala	Val	Phe	Pro	Pro	Leu	Ala	Ser	Asp	Glu	Ala													
2210					2220					2230					2240					2250									
GGC	AAC	GTC	ACG	CTC	AAC	ATG	TCT	GAC	GGG	CTA	TAT	ACT	AAG	GAC	AAC	AAG													
Gly	<u>Asn</u>	<u>Val</u>	<u>Thr</u>	Leu	<u>Asn</u>	<u>Met</u>	<u>Ser</u>	Asp	Gly	Leu	Tyr	Thr	Lys	Asp	Asn	Lys													
2260					2270					2280					2290					2300									
CTA	GCT	GTC	AAA	GTA	GGT	CCC	GGG	CTG	TCC	CTC	GAC	TCC	AAT	AAT	GCT	CTC													
Leu	Ala	Val	Lys	Val	Gly	Pro	Gly	Leu	Ser	Leu	Asp	Ser	Asn	Asn	Ala	Leu													
2310					2320					2330					2340					2350									
CAG	GTC	CAC	ACA	GGC	GAC	GGG	CTC	ACG	GTA	ACC	GAT	GAC	AAG	GTG	TCT	CTA													
Gln	Val	His	Thr	Gly	Asp	Gly	Leu	Thr	Val	Thr	Asp	Asp	Lys	Val	Ser	Leu													
2360					2370					2380					2390					2400									
AAT	ACC	CAA	GCT	CCC	CTC	TCG	ACC	ACC	AGC	GCG	GGC	CTC	TCC	CTA	CTT	CTG													
Asn	Thr	Gln	Ala	Pro	Leu	Ser	Thr	Thr	Ser	Ala	Gly	Leu	Ser	Leu	Leu	Leu													
2410					2420					2430					2440					2450					2460				
GGT	CCC	AGC	CTC	CAC	TTA	GGT	GAG	GAG	GAA	CGA	CTA	ACA	GTA	AAC	ACC	GGA													
Gly	Pro	Ser	Leu	His	Leu	Gly	Glu	Glu	Glu	Arg	Leu	Thr	Val	Asn	Thr	Gly													
2470					2480					2490					2500					2510									
GCG	GGC	CTC	CAA	ATT	AGC	AAT	AAC	GCT	CTG	GCC	GTA	AAA	GTA	GGT	TCA	GGT													
Ala	Gly	Leu	Gln	Ile	Ser	Asn	Asn	Ala	Leu	Ala	Val	Lys	Val	Gly	Ser	Gly													
2520					2530					2540					2550					2560									
ATC	ACC	GTA	GAT	GCT	CAA	AAC	CAG	CTC	GCT	GCA	TCC	CTG	GGG	GAC	GGT	CTA													
Ile	Thr	Val	Asp	Ala	Gln	Asn	Gln	Leu	Ala	Ala	Ser	Leu	Gly	Asp	Gly	Leu													
2570					2580					2590					2600					2610									
GAA	AGC	AGA	GAT	<u>AAT</u>	<u>AAA</u>	ACT	GTC	GTT	AAG	GCT	GGG	CCC	GGA	CTT	ACA	ATA													
Glu	Ser	Arg	Asp	<u>Asn</u>	<u>Lys</u>	<u>Thr</u>	Val	Val	Lys	Ala	Gly	Pro	Gly	Leu	Thr	Ile													
2620					2630					2640					2650					2660									
ACT	AAT	CAA	GCT	CTT	ACT	GTT	GCT	ACC	GGG	AAC	GGC	CTT	CAG	GTC	AAC	CCG													
Thr	Asn	Gln	Ala	Leu	Thr	Val	Ala	Thr	Gly	Asn	Gly	Leu	Gln	Val	Asn	Pro													

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2670	2680	2690	2700	2710
GAA GGG CAA CTG CAC CTA AAC ATT ACT GCC GGT CAG GGC CTC AAC TTT GCA				
Glu Gly Gln Leu Gln Leu <u>Asn Ile Thr</u> Ala Gly Gln Gly Leu Asn Phe Ala				
2720	2730	2740	2750	2760
AAC AAC AGC CTC GCC GTG GAG CTG GGC TCG GGC CTG CAT TTT CCC CCT GGC				
<u>Asn Asn Ser</u> Leu Ala Val Glu Leu Gly Ser Gly Leu His Phe Pro Pro Gly				
2770	2780	2790	2800	2810
CAA AAC CAA GTA AGC CTT TAT CCC GGA GAT GGA ATA GAC ATC CGA GAT AAT				
Gln Asn Gln Val Ser Leu Tyr Pro Gly Asp Gly Ile Asp Ile Arg Asp Asn				
2820	2830	2840	2850	2860
AGG GTG ACT GTG CCC GCT GGG CCA GGC CTG AGA ATG CTC AAC CAC CAA CTT				
Arg Val Thr Val Pro Ala Gly Pro Gly Leu Arg Met Leu Asn His Gln Leu				
2870	2880	2890	2900	2910
GCC GTA GCT TCC GGA GAC GGT TTA GAA GTC CAC AGC GAC ACC CTC CGG TTA				
Ala Val Ala Ser Gly Asp Gly Leu Glu Val His Ser Asp Thr Leu Arg Leu				
2920	2930	2940	2950	2960
AAG CTC TCC CAC GGC CTG ACA TTT GAA AAT GGC GCC GTA CGA GCA AAA CTA				
Lys Leu Ser His Gly Leu Thr Phe Glu Asn Gly Ala Val Arg Ala Lys Leu				
2980	2990	3000	3010	3020
GGA CCA GGA CTT GGC ACA GAC GAC TCT GGT CGG TCC GTG GTT CGC ACA GGT				
Gly Pro Gly Leu Gly Thr Asp Asp Ser Gly Arg Ser Val Val Arg Thr Gly				
3030	3040	3050	3060	3070
CGA GGA CTT AGA GTT GCA AAC GGC CAA GTC CAG ATC TTC AGC GGA AGA GGC				
Arg Gly Leu Arg Val Ala Asn Gly Gln Val Gln Ile Phe Ser Gly Arg Gly				
3080	3090	3100	3110	3120
ACC GCC ATC GGC ACT GAT AGC AGC CTC ACT CTC AAC ATC CGG GCG CCC CTA				
Thr Ala Ile Gly Thr Asp Ser Ser Leu Thr Leu Asn Ile Arg Ala Pro Leu				
3130	3140	3150	3160	3170
CAA TTT TCT GGA CCC GCC TTG ACT GCT AGT TTG CAA GGC AGT GGT CCG ATT				
Gln Phe Ser Gly Pro Ala Leu Thr Ala Ser Leu Gln Gly Ser Gly Pro Ile				
3180	3190	3200	3210	3220
ACT TAC AAC AGC AAC AAT GGC ACT TTC GGT CTC TCT ATA GGC CCC GGA ATG				
Thr Tyr Asn Ser Asn <u>Asn Gly Thr</u> Phe Gly Leu Ser Ile Gly Pro Gly Met				
3230	3240	3250	3260	3270
TGG GTA GAC CAA AAC AGA CTT CAG GTA AAC CCA GGC GCT GGT TTA GTC TTC				
Trp Val Asp Gln Asn Arg Leu Gln Val Asn Pro Gly Ala Gly Leu Val Phe				
3280	3290	3300	3310	3320
CAA GGA AAC AAC CTT GTC CCA AAC CTT GCG GAT CCG CTG GCT ATT TCC GAC				
Gln Gly Asn Asn Leu Val Pro Asn Leu Ala Asp Pro Leu Ala Ile Ser Asp				
3330	3340	3350	3360	3370
AGC AAA ATT AGT CTC AGT CTC GGT CCC GGC CTG ACC CAA GCT TCC AAC GCC				
Ser Lys Ile Ser Leu Ser Leu Gly Pro Gly Leu Thr Gln Ala Ser Asn Ala				

3380 3390 3400 3410 3420  
 CTG ACT TTA AGT TTA GGA AAC GGG CTT GAA TTC TCC AAT CAA GCC GTT GCT  
 Leu Thr Leu Ser Leu Gly Asn Gly Leu Glu Phe Ser Asn Gln Ala Val Ala

3430 3440 3450 3460 3470 3480  
 ATA AAA GCG GGC CGG GGC TTA CGC TTT GAG TCT TCC TCA CAA GCT TTA GAG  
 Ile Lys Ala Gly Arg Gly Leu Arg Phe Glu Ser Ser Ser Gln Ala Leu Glu

3490 3500 3510 3520 3530  
 AGC AGC CTC ACA GTC GGA AAT GGC TTA ACG CTT ACC GAT ACT GTG ATC CGC  
 Ser Ser Leu Thr Val Gly Asn Gly Leu Thr Leu Thr Asp Thr Val Ile Arg

3540 3550 3560 3570 3580  
 CCC AAC CTA GGG GAC GGC CTA GAG GTC AGA GAC AAT AAA ATC ATT GTT AAG  
 Pro Asn Leu Gly Asp Gly Leu Glu Val Arg Asp Asn Lys Ile Ile Val Lys

3590 3600 3610 3620 3630  
 CTG GGC GCG AAT CTT CGT TTT GAA AAC GGA GCC GTA ACC GCC GGC ACC GTT  
 Leu Gly Ala Asn Leu Arg Phe Glu Asn Gly Ala Val Thr Ala Gly Thr Val

3640 3650 3660 3670 3680  
 AAC CCT TCT GCG CCC GAG GCA CCA CCA ACT CTC ACT GCA GAA CCA CCC CTC  
Asn Pro Ser Ala Pro Glu Ala Pro Pro Thr Leu Thr Ala Glu Pro Pro Leu

3690 3700 3710 3720 3730  
 CGA GCC TCC AAC TCC CAT CTT CAA CTG TCC CTA TCG GAG GGC TTG GTT GTG  
 Arg Ala Ser Asn Ser His Leu Gln Leu Ser Leu Ser Glu Gly Leu Val Val

3740 3750 3760 3770 3780  
 CAT AAC AAC GCC CTT GCT CTC CAA CTG GGA GAC GGC ATG GAA GTA AAT CAG  
 His Asn Asn Ala Leu Ala Leu Gln Leu Gly Asp Gly Met Glu Val Asn Gln

3790 3800 3810 3820 3830  
 CAC GGA CTT ACT TTA AGA GTA GGC TCG GGT TTG CAA ATG CGT GAC GGC ATT  
 His Gly Leu Thr Leu Arg Val Gly Ser Gly Leu Gln Met Arg Asp Gly Ile

3840 3850 3860 3870 3880  
 TTA ACA GTT ACA CCC AGC GGC ACT CCT ATT GAG CCC AGA CTG ACT GCC CCA  
 Leu Thr Val Thr Pro Ser Gly Thr Pro Ile Glu Pro Arg Leu Thr Ala Pro

3890 3900 3910 3920 3930  
 CTG ACT CAG ACA GAG AAT GGA ATC GGG CTC GCT CTC GGC GCC GGC TTG GAA  
 Leu Thr Gln Thr Glu Asn Gly Ile Gly Leu Ala Leu Gly Ala Gly Leu Glu

3940 3950 3960 3970 3980 3990  
 TTA GAC GAG AGC GCG CTC CAA GTA AAA GTT GGG CCC GGC ATG CGC CTG AAC  
 Leu Asp Glu Ser Ala Leu Gln Val Lys Val Gly Pro Gly Met Arg Leu Asn

4000 4010 4020 4030 4040  
 CCT GTA GAA AAG TAT GTA ACC CTG CTC CTG GGT CCT GGC CTT AGT TTT GGG  
 Pro Val Glu Lys Tyr Val Thr Leu Leu Leu Gly Pro Gly Leu Ser Phe Gly

4050 4060 4070 4080 4090  
 CAG CCG GCC AAC AGG ACA AAT TAT GAT GTG CGC GTT TCT GTG GAG CCC CCC  
 Gln Pro Ala Asn Arg Thr Asn Tyr Asp Val Arg Val Ser Val Glu Pro Pro



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4100 ATG GTT TTC GGA C Met Val Phe Gly Gln	4110 CGT GGT CAG CTC Arg Gly Gln Leu	4120 ACA TTT TTT Thr Phe Leu	4130 GTG GGT CAC GGA Val Gly His Gly	4140 CTA Leu
4150 CAC ATT CAA AAT TCC His Ile Gln Asn Ser	4160 AAA CTT CAG CTC Lys Leu Gln Leu	4170 AAT TTG GGA CAA GGC Asn Leu Gly Gln Gly	4180 CTC AGA ACT Leu Arg Thr	4190 ACT
4200 GAC CCC GTC ACC AAC Asp Pro Val Thr Asn	4210 CAG CTG GAA GTG Gln Leu Glu Val	4220 CCC CTC GGT CAA GGT Pro Leu Gly Gln Gly	4230 TTG GAA ATT Leu Glu Ile	4240 ATT
4250 GCA GAC GAA TCC CAG Ala Asp Glu Ser Gln	4260 GTT AGG GTT AAA TTG Val Arg Val Lys Leu	4270 GTC GGC GAT GGC Gly Asp Gly Leu	4280 CTG CAG TTT GAT Gln Phe Asp	4290 GAT
4300 TCA CAA GCT CGC ATC Ser Gln Ala Arg Ile	4310 ACT ACC GCT CCT AAC Thr Thr Ala Pro Asn	4320 ATG GTC ACT GAA ACT Met Val Thr Glu	4330 CTG TGG Thr Leu Trp	4340 TGG
4350 ACC GGA ACA GGC AGT Thr Gly Thr Gly Ser	4360 AAT GCT AAT GTT ACA Asn Ala Asn Val Thr	4370 TGG CGG GGC TAC Trp Arg Gly Tyr	4380 ACT GCC CCC Thr Ala Pro	4390 CCC
4400 GGC AGC AAA CTC TTT Gly Ser Lys Leu Phe	4410 TTG AGT CTC ACT Leu Ser Leu Thr	4420 CGG TTC AGC ACT Arg Phe Ser Thr	4430 GGT CTA GTT TTA Gly Leu Val Leu	4440 TTA
4450 GGA AAC ATG ACT ATT Gly Asn Met Thr Ile	4460 GAC AGC AAT GCA TCC Asp Ser Asn Ala Ser	4470 TTT GGG CAA TAC Phe Gly Gln Tyr	4480 ATT AAC GCG Ile Asn Ala	4490 GCG
4510 GGA CAC GAA CAG ATC Gly His Glu Gln Ile	4520 GAA TGC TTT ATA TTG Glu Cys Phe Ile Leu	4530 TTG GAC AAT CAG GGT Leu Asp Asn Gln Gly	4540 AAC CTA Asn Leu	4550 CTA
4560 AAA GAA GGA TCT AAC Lys Glu Gly Ser Asn	4570 TTG CAA GGC ACT TGG Leu Gln Gly Thr Trp	4580 GAA GTG AAG AAC AAC Glu Val Lys Asn Asn	4590 CCC TCT Pro Ser	4600 TCT
4610 GCT TCC AAA GCT GCT Ala Ser Lys Ala Ala	4620 TTT TTG CCT TCC ACC Phe Leu Pro Ser Thr	4630 GCC CTA TAC CCC Ala Leu Tyr Pro	4640 ATC CTC AAC Ile Leu Asn	4650 AAC
4660 GAA AGC CGA GGG AGT Glu Ser Arg Gly Ser	4670 CTT CCT GGA AAA AAT Leu Pro Gly Lys Asn	4680 CTT GTG GGC ATG CAA Leu Val Gly Met Gln	4690 GCC ATA Ala Ile	4700 ATA
4710 CTG GGA GGC GGG GGC Leu Gly Gly Gly Gly	4720 ACT TGC ACT GTG ATA Thr Cys Thr Val Ile	4730 GCC ACC CTC AAT GGC Ala Thr Leu Asn Gly	4740 AGA CGC Arg Arg	4750 CGC
4760 AGC AAC AAC TAT CCC Ser Asn Asn Tyr Pro	4770 GCG GGC CAG TCC ATA Ala Gly Gln Ser Ile	4780 ATT TTC GTG TGG CAA Ile Phe Val Trp Gln	4790 GAA TTC Glu Phe	4800 TTC

4810	482	4830	484	4850	
AAC ACC ATA GCC CAA CCT CTG AAC CAC TCT ACA CTT ACT TTT TCT TAC					
Asn Thr Ile Ala Arg Gln Pro Leu <u>Asn His Ser</u> Thr Leu Thr Phe Ser Tyr					
4860	4870	4880	4890	4900	
TGG ACT TA AAT AAG TTG GAA <u>ATA AAG</u> AGT TAA ACT GAA TGT TTA AGT GCA					
Trp Thr					
4910	4920	4930	4940	4950	
ACA GAC TTT TAT TGG TTT TGG CTC ACA ACA AAT TAC AAC AGC ATA GAC AAG					
4960	4970	4980	4990	5000	
TCA TAC CGG TCA AAC AAC ACA GGC TCT CGA AAA CGG GCT <u>AAC</u> CGC TCC AAG					
5010	5020	5030	5040	5050	5060
AAT CTG TCA CGC AGA CGA GCA AGT CCT AAA TGT TTT TTC ACT CTC TTC GGG					
	5070	5080	5090	5100	
GCC AAG TTC AGC ATG TAT CGG ATT TTC TGC TTA CAC CTT T					

[illegible]

FIGURE 8(a)

FIGURE 8(b)

BAV3 - MKRSVPQD--FNLVYPYKAKR-----PNIMPPFFDRNGFVENQEATLAML -43  
Ad2 - MKRARPS EDTFN PVYPYDTETGPPTVPF LTPPFVSPNGFQESPPGVLSLR -50  
BAV3 - VEKPLTFDKE-GALT LGVGRGIRINPAGLLETNDLASAVFPPLASDEAGN -92  
Ad2 - VSEPL--DTSHGMLALKMGSGLTLDKAGNLT SQNVTTV----- -86  
BAV3 - VTLNMSDGLYTKDNKLAVKVGPGLSLDSNNALQVHTGDGLTVTDDKVSLN -142  
Ad2 - -----TQPLKKT KSNISLDT SAPLTI-TSGALT VATTAPLIVTSGALSVQ -130  
BAV3 - TQAPLSTTSAGLSLLLGP SLHLGEEERLT VNTGAGLQISNNALAVKVGSG -192  
Ad2 - SQAPLT-----VQDSKLSIATKGPITVSDGKLALQTSAP -164  
BAV3 - ITVDAQNQLAASLG DGLES RDNKT VVKAGPGLTITNQALT VATGNGLQVN -242  
Ad2 - LSGSDSDTLTVT-----ASPPLTTATGS-LGIN -191  
BAV3 - PEGQLQLNITAGQGLNFANNSLAVELGSGLHFPFGQNQVSLYPGDGIDIR -292  
Ad2 - MEDPIYVN-----NGKIGIKISGPLQVAQ----- -215  
BAV3 - DNRVTVPAGPGLRMLNHQLAVASGDGLEVHSDTLRLKLSHGLTFENGAVR -342  
Ad2 - -----NSDTLTVVTGPGVTVEQNSLR -236  
BAV3 - AKLGPG LGTDDSGRSVVRTGRGLRVANGQVQIFSGRGTAIGTDSSLT LNI -392  
Ad2 - TKVAGAIGYDSSNNMEIKTGGGMRINN L--LILDVDYPFDAQTKLRLKL -284  
BAV3 - RAPLQFSGPALTASLQSGSPITYNSNNGTFGLSIGPGMWVDQNRLQVNPG -442  
Ad2 - -----GQGPLYINASHN-----LDINYN -302  
BAV3 - AGLVFQGNLVPNLADPLAISDSKISLSLGPGLTQASNALTSLGNGLEF -492  
Ad2 - RGLYL-----FNASNNTKKLEVS IKKSS-----GLNF -329  
BAV3 - SNQAVAIKAGRGLRFESSSQALESSLTVGNGLTLTDTVIRPNLGDGLEVR -542  
Ad2 - DNTAIAINAGKGLEFDNT----- -348  
BAV3 - DNKIIVKLGANLRFENGAVTAGTVNP SAPEAPPTLTAEPPLRASN SHLQL -592  
Ad2 - ----- -348  
BAV3 - SLSEGLVVHNNALALQLGDGMEVNQHGLTLRVGSGLQMRDGILTVTPSGT -642  
Ad2 - -----SESPDIN--PIKTKIGSGID-----YNENGA -372

FIGURE 8(c)-1

BAV3 - PIEPRLTAPLTQTENGIGLALGAGLELDESALQVKVGPGMRLNPVEKYVT -692  
Ad2 - MIT-----KLGAGLSFDNSG----- -387  
BAV3 - LLLGPGLSFGQPANRTNYDVRVSVEPPMVFGQRGQLTFLVGHGLHIONSK -742  
Ad2 - -----AITIG-----NKNDCKLTLTWTTDPDSP-----NCR -412  
BAV3 - LQLNLGQGLRTDPVTNQLEVP LGQGLEIADESQVRVKLG DGLOFDSQARI -792  
Ad2 - IHSD-----NDCKFTLVLT---KCGSQVLA -434  
BAV3 - TTAPNMVTETLWTGTGSNANVTWRGYTAPGSKLFLSLTRFSTGLVLGNMT -842  
Ad2 - TVAALAVSGDLSSMTGTVASVS-----IFLRFDQ--NGVLMENSS -472  
BAV3 - IDSNASFGQYINAGHEQIECFILLDNQGNLKEGSNLQGTWEVKNNPSASK -892  
Ad2 - LKKHY-----WNERNGNS-----TNANPYTNA -494  
BAV3 - AAFLPSTALYPILNESRGSLPGKNLVGMQAILGGGGTCTVIA-TLNGRRS -941  
Ad2 - VGFM PNLLAYP---KTQSQTAKNNIVSQVYLHGDKTKPMILTITLNGTSE -541  
BAV3 - NNYPAGQSII---FVWQ-EFNTIARQPLNHSTLTFSYWT -976  
Ad2 - STETSEVSTYSMSFTWSWESGKYTTETTFATNSYTF SYIAQE -582

FIGURE 8(c)-2

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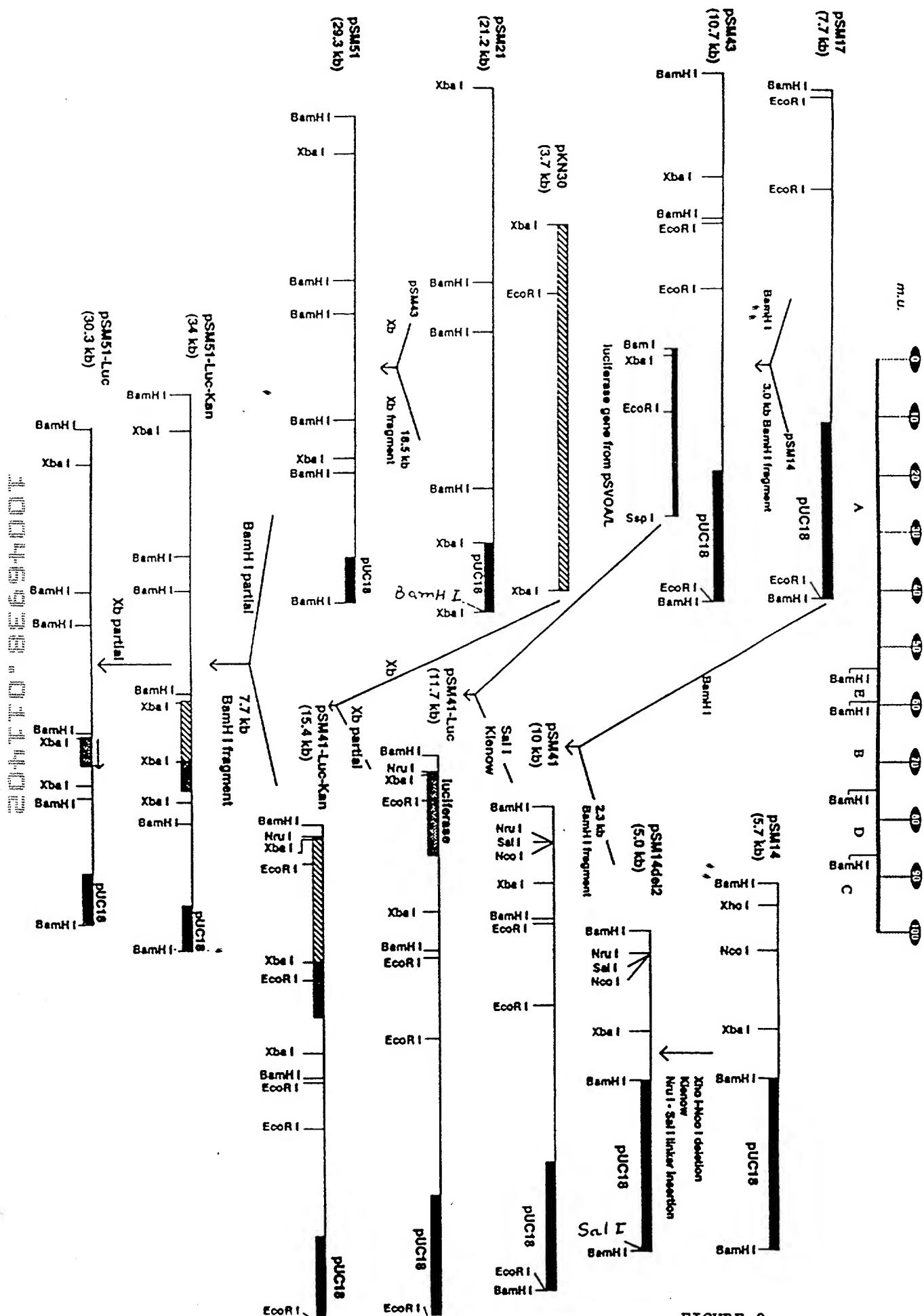
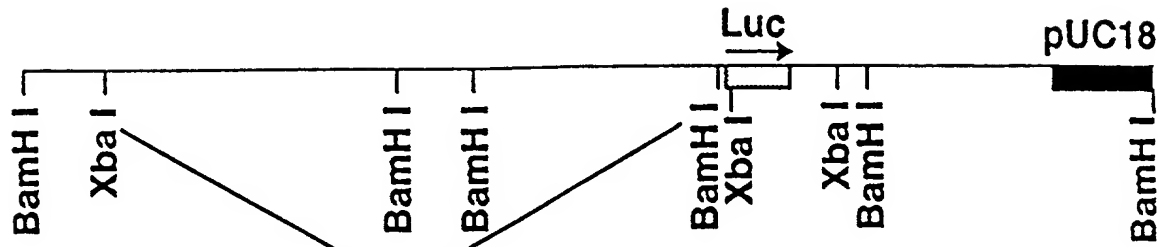
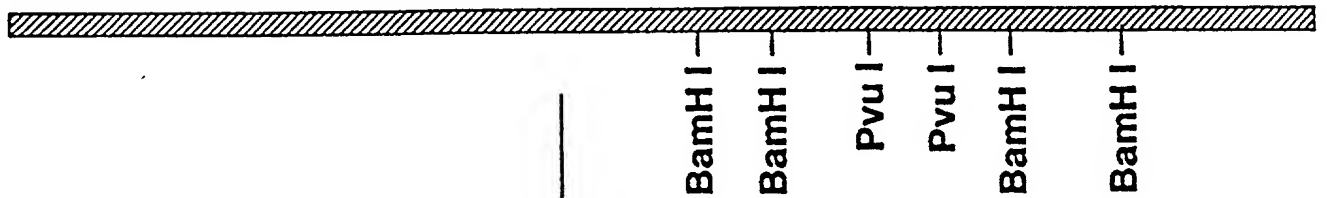


FIGURE 9

pSM51-Luc  
(30.3 Kb)



wt BAd3  
(35 Kb)



Cotransfection



BAd3-Luc  
(36 Kb)

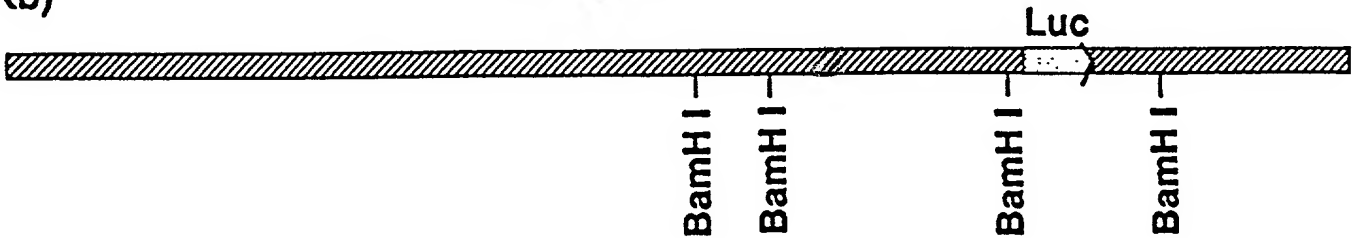
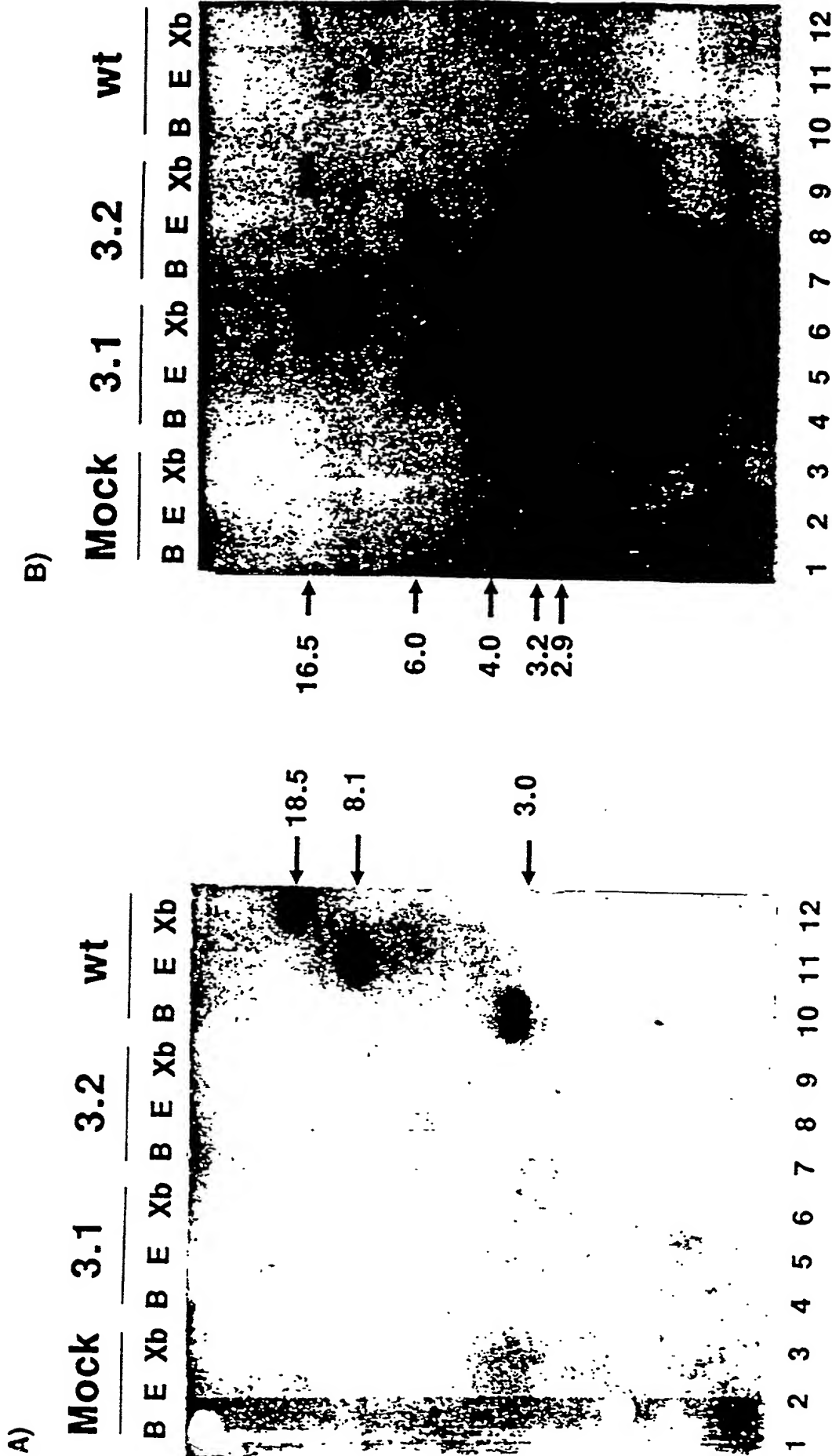


FIGURE 10





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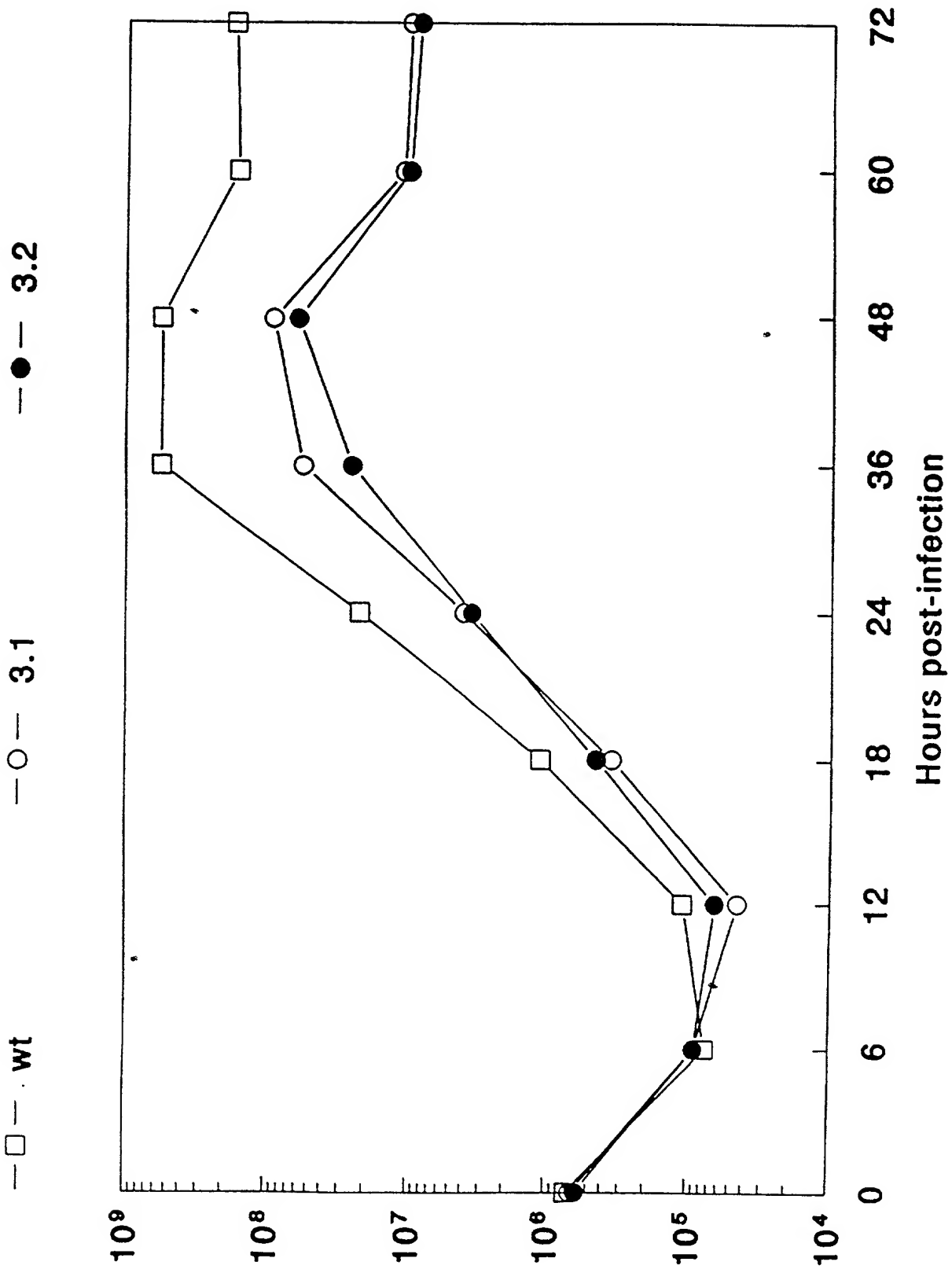
Title: RECOMBINANT PROTEIN PRODUCTION IN BOVINE  
ADENOVIRUS EXPRESSION VECTOR SYSTEM

Inventor: Suresh K. MITTAL et al.

Application No.: To Be Assigned

Docket No.: 293102002103

Virus titer/ $4 \times 10^6$  cells



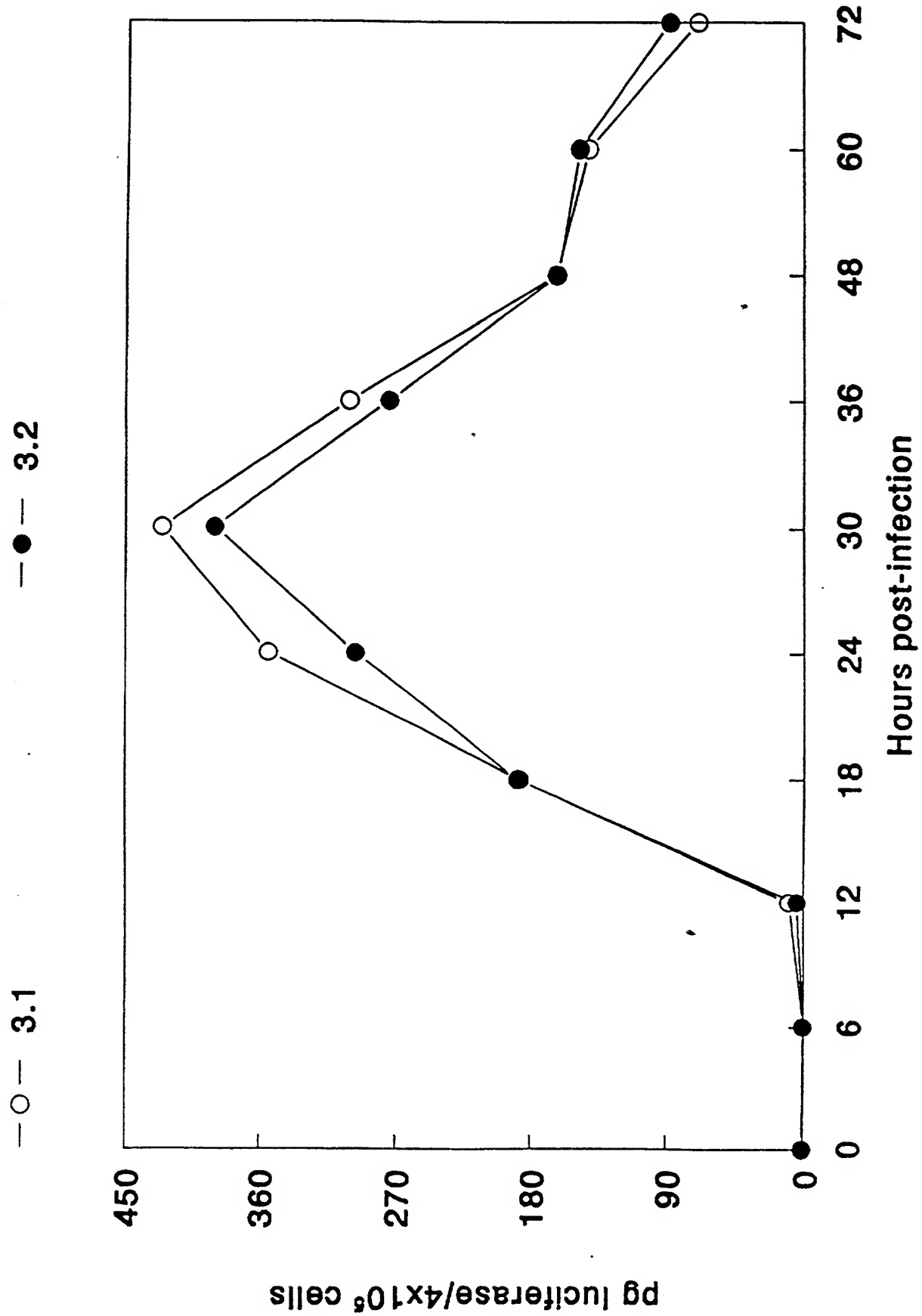
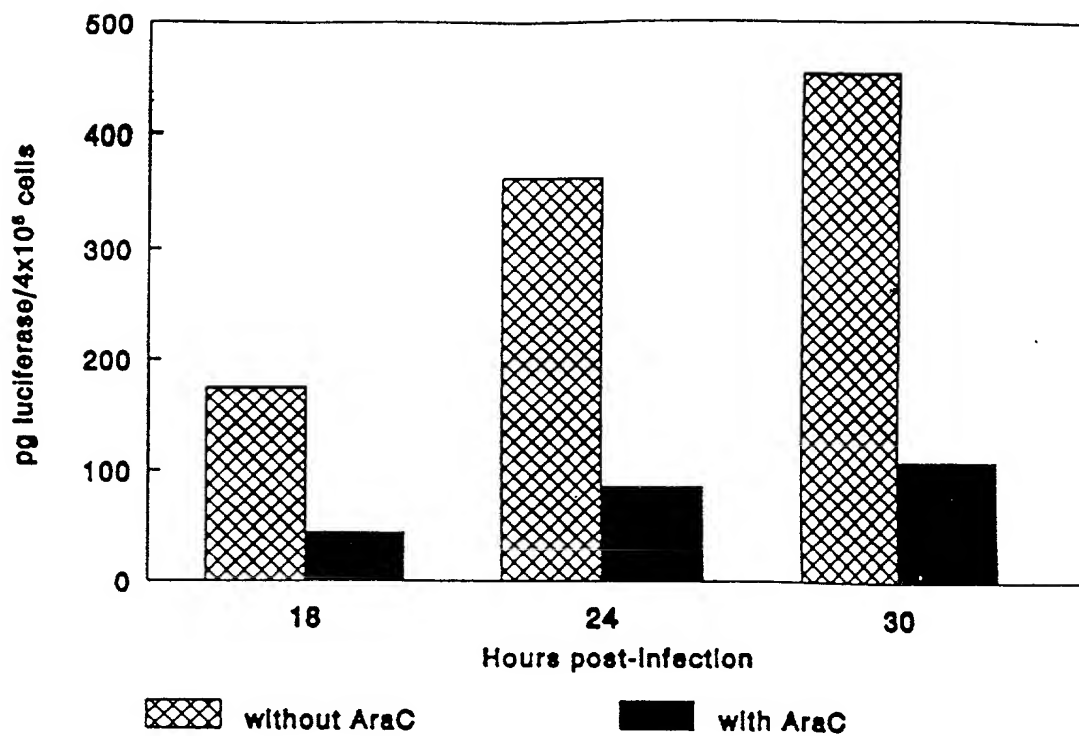


FIGURE 13

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A)



B)

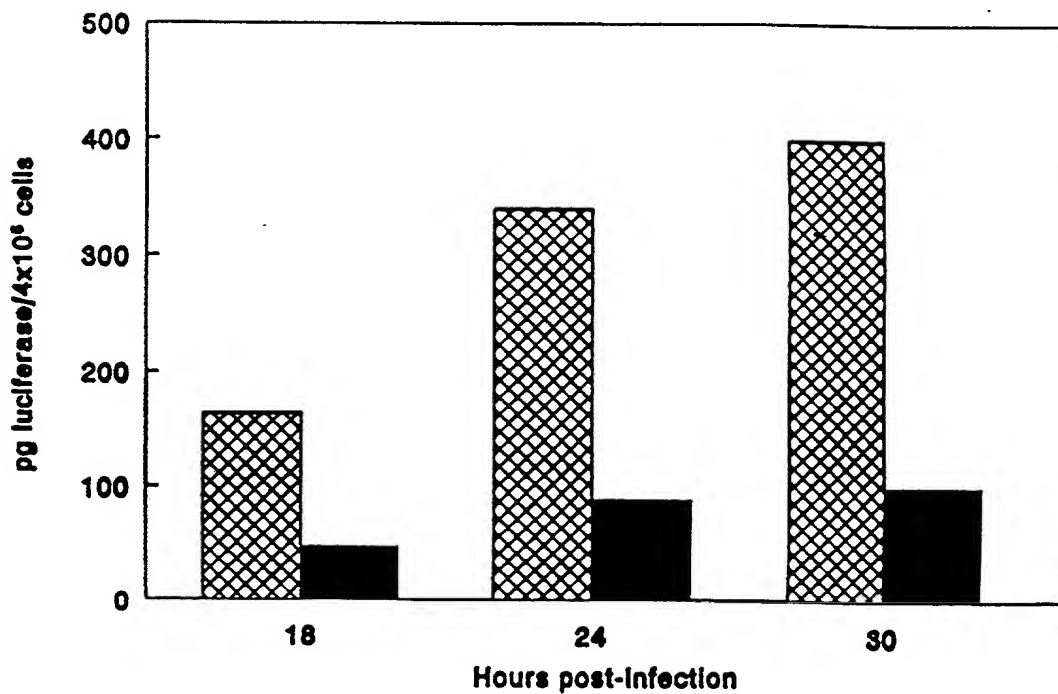
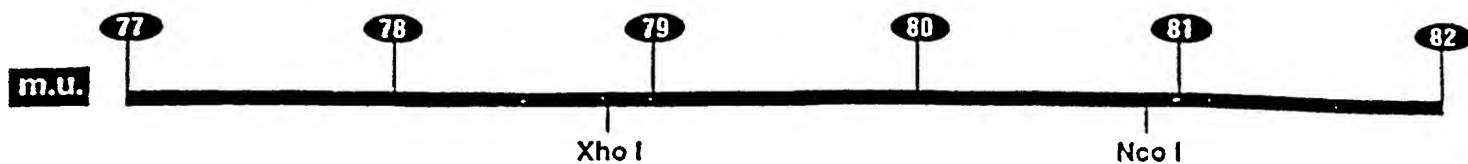
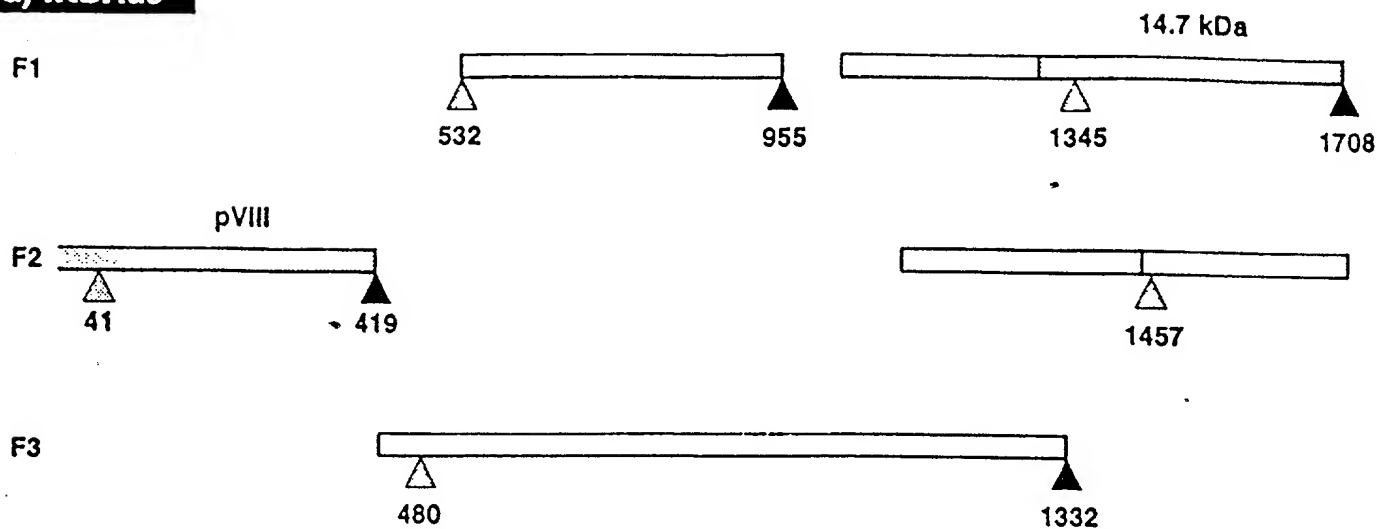


FIGURE 14



### a) wtBAd3



### b) BAd3-Luc

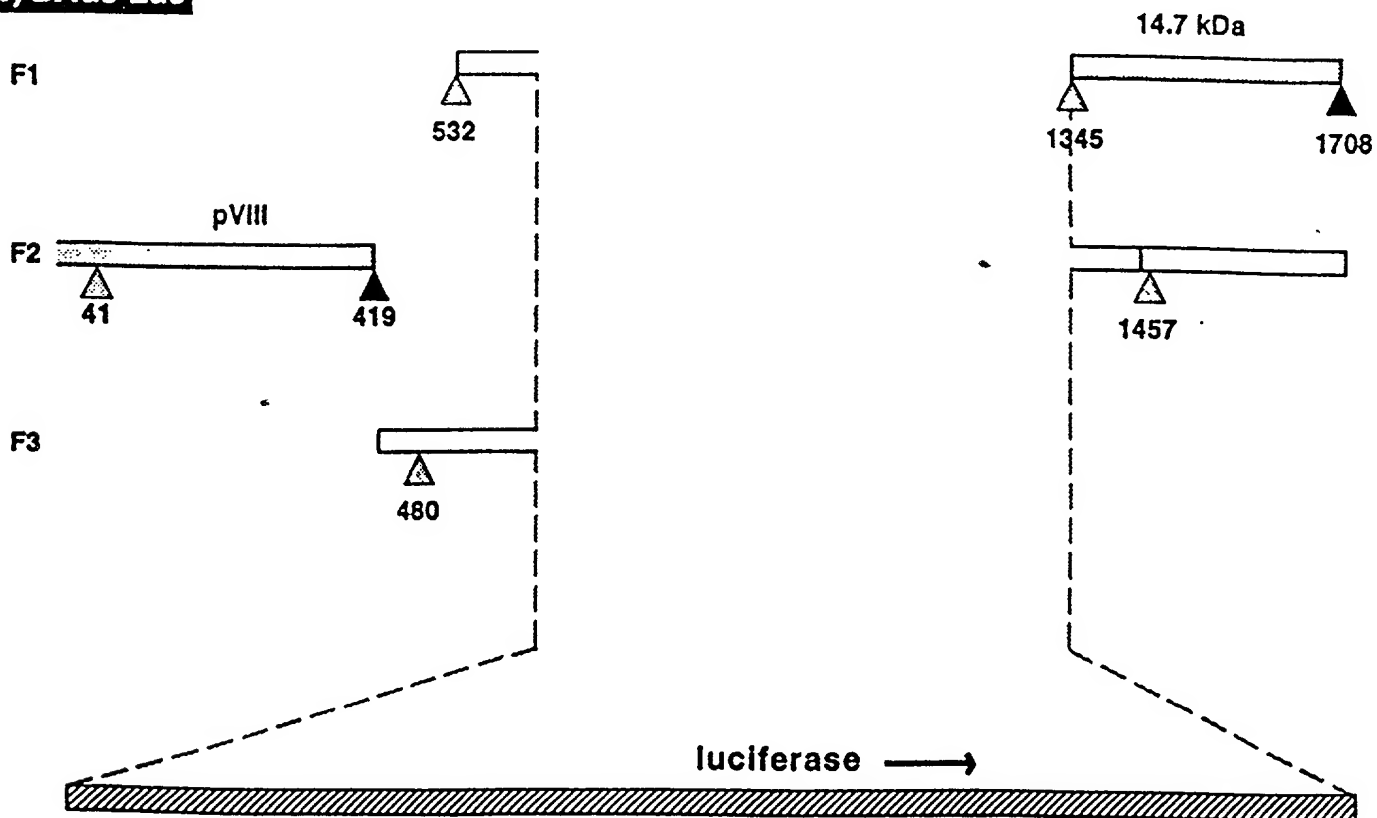


FIGURE 15

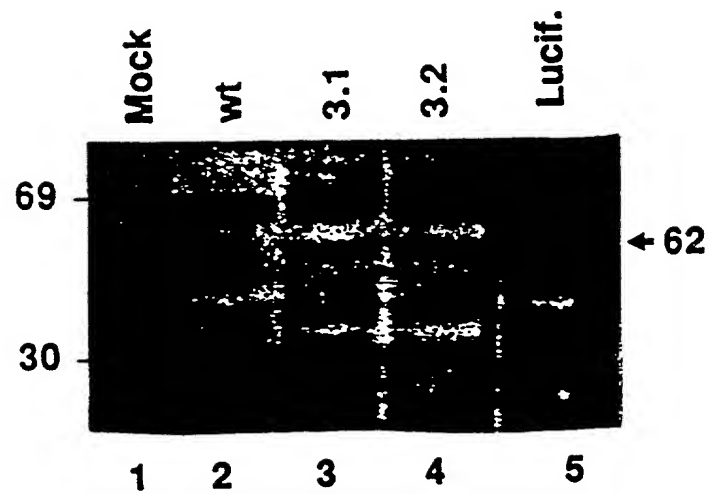
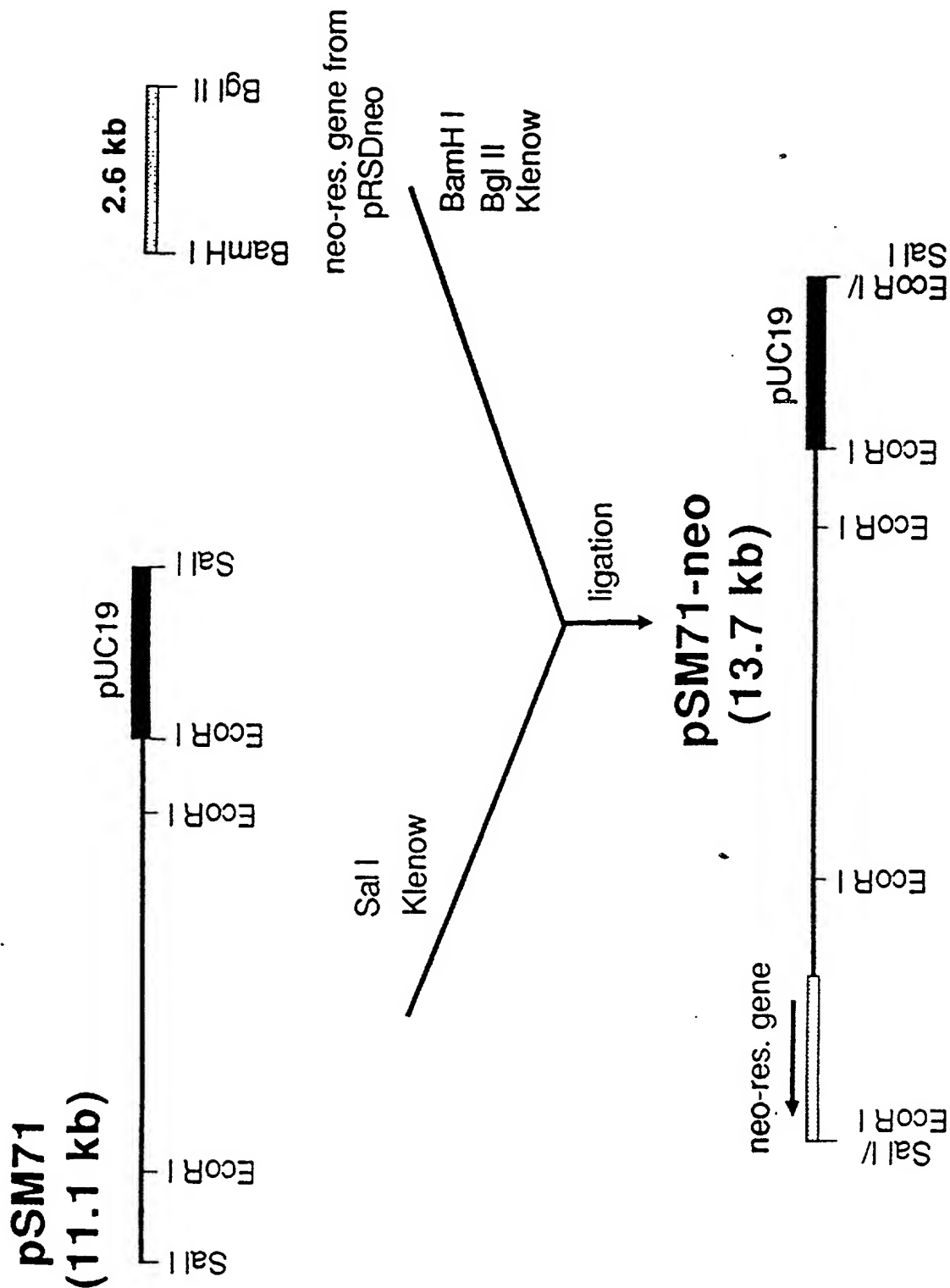
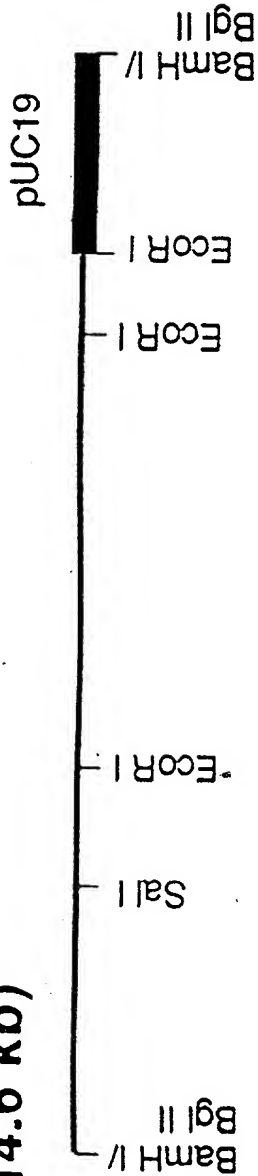


FIGURE 16



**pSM61**  
(14.6 kb)



Sheet 32 of 33

pKN30 containing  
neo-res. gene

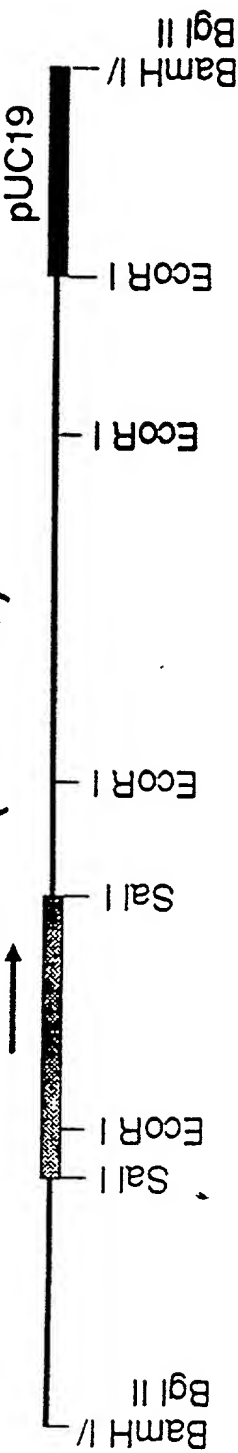
Sal I

FIGURE 18

ligation

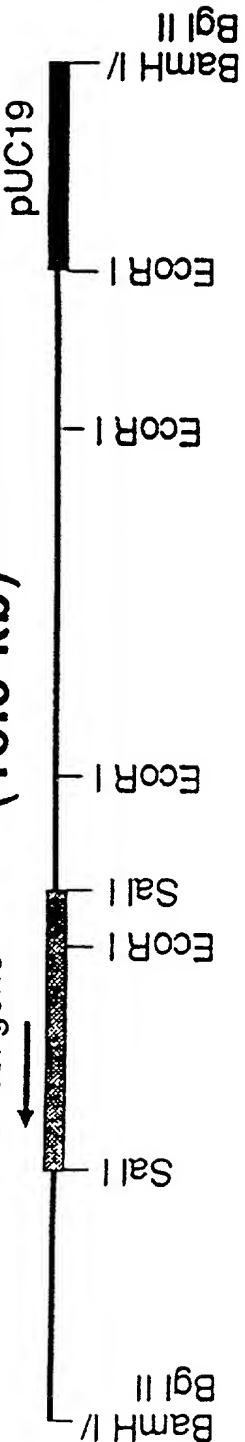
**pSM61-kan1**  
(18.3 kb)

neo-res. gene



**pSM61-kan2**  
(18.3 kb)

neo-res. gene





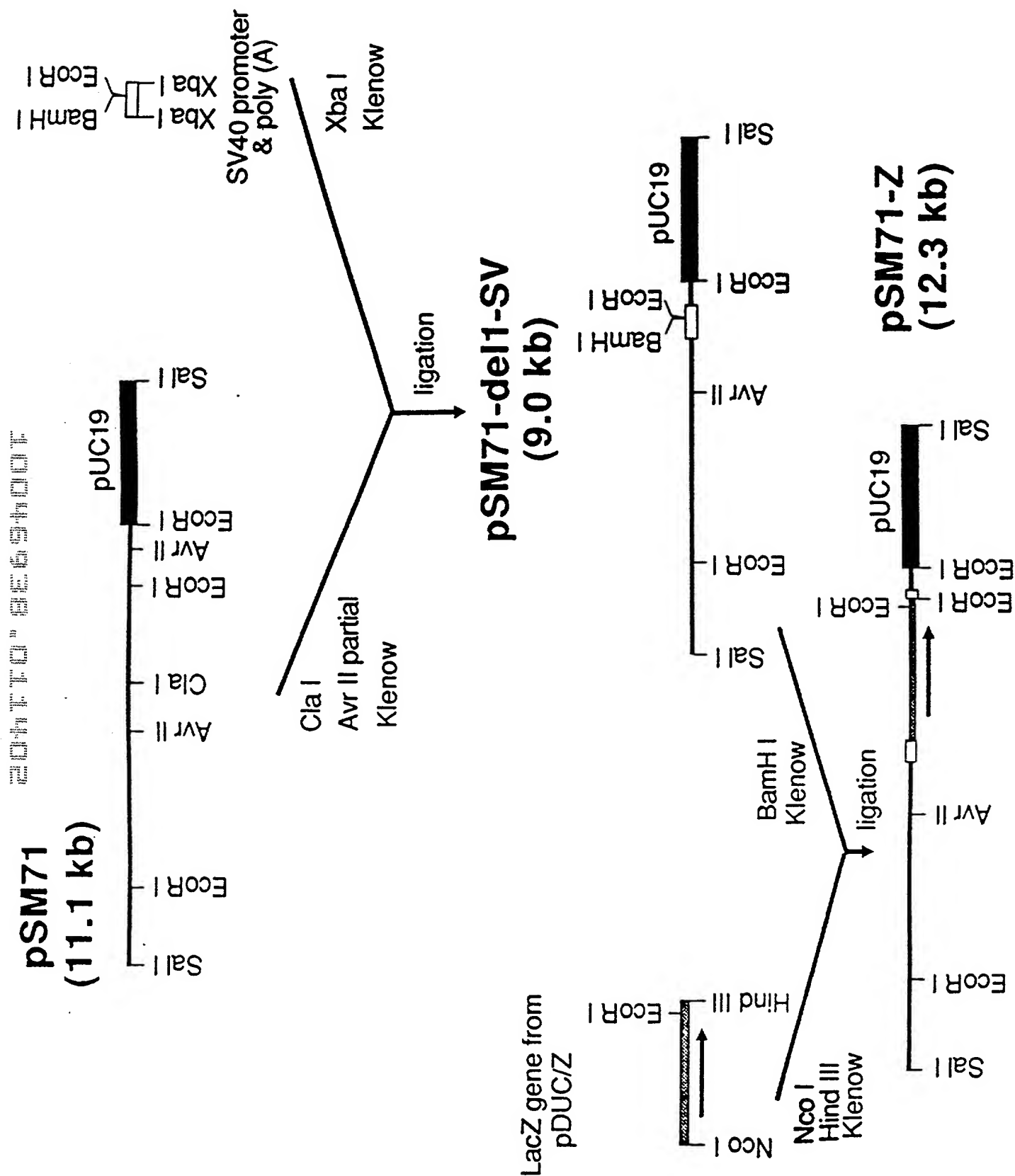


FIGURE 19